

#### IN THE SPECIFICATION:

Please replace the paragraph at page 12, lines 15-23 as follows:

**FIGURE 4** depicts the comparison between the murine (SEQ ID NO:2) and human (SEQ ID NO:4) deduced amino acid sequences. The sequence of the human OB deduced amino acid sequence was highly homologous to that of mouse. Conservative changes are noted by a dash, and non-conservative changes by an asterisk. The variable glutamine codon is underlined, as is the position of the nonsense mutation in C57BL/6J *ob/ob* (1J) mice. Overall, there is 83% ~~84%~~ identity at the amino acid level, although only nine ~~six~~ substitutions were found between the valine at codon 22 (immediately downstream of the signal sequence) and the cysteine at position 117.

Please replace the paragraph at page 102, lines 8-20 as follows:

Human fat tissue RNA was analyzed on Northern blots, RNA species of a similar size to the mouse *OB* gene was detected. Sequencing and analysis of cDNA clones revealed that human *OB* also encodes a 167 amino acid polypeptide (Figure 2A and B and Figure 3). Two classes of cDNA, with or without three base pair deletions, were found in human as well (Figure 6). The mouse and human *OB* genes were highly homologous in the predicted coding region, but had only 30% homology in the available 3' and 5' untranslated regions. An N-terminal signal sequence was also present in the human OB polypeptide. Comparison of the human and mouse OB polypeptide sequences showed that the two molecules share an overall 83% ~~84%~~ identity at the amino acid level (Figure 4). The N-termini of the mature proteins from both species share even higher homology, with only six ~~four~~ conservative and six ~~three~~ nonconservative amino acid substitutions among the N-terminal 100 amino acid residues.